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OM protein - nucleic search, using frame_plus_p2n model

                              GenCore version 5.1.3
                              Copyright (c) 1993 - 2002 Compugen Ltd.

Run on:           December  9, 2002, 10:46:24 ; Search time 61 Seconds
                                                 (without alignments)
                                                 2135.042 Million cell updates/sec

Title:            US-09-765-034-2
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Perfect score:    1747

Scoring table:    BLOSUM62
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                  Ygapop  10.0 , Ygapext  0.5
                  Fgapop   6.0 , Fgapext  7.0
                  Delop    6.0 , Delext   7.0

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Searched:         350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters:       700850

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :    Published_Applications

Command line parameters:
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-Q-/cgn2_1/USPTO_spool/US09765034/runat_05122002_132013_21353/app_query.fasta_1.519
-DB=Published_Applications_NA -QFMT=fastap -SUFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09765034 @CGN_1_1_21 @runat_05122002_132013_21353
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_NMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Published_Applications_NA:*
 1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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 5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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 7:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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 9:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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12:  /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	477	27.3	1014	10	US-09-943-798-3	Sequence 3, Appli
2	395.5	22.6	831	10	US-09-943-798-1	Sequence 1, Appli
3	384	22.0	993	10	US-09-826-791-1	Sequence 1, Appli
4	384	22.0	1041	9	US-09-828-478-1	Sequence 1, Appli

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 5    384   22.0  1041  10   US-09-826-791-5    Sequence 5, Appli
 6    384   22.0  1041  10   US-09-866-230-6    Sequence 6, Appli
 7    384   22.0  1430  10   US-09-828-478-3    Sequence 3, Appli
 8    346.5 19.8  1700  10   US-09-728-952-26   Sequence 26, Appli
 9    338   19.3  1313  10   US-09-728-422-1    Sequence 1, Appli
10    338   19.3  1020  10   US-09-788-133-1    Sequence 1, Appli
11    336.5 19.3  1068  10   US-09-880-107-3034 Sequence 3034, App
12    336.5 19.3  1422  10   US-09-864-761-26799 Sequence 26799, A
13    331   18.9  1933   9   US-09-864-761-10158 Sequence 10158, A
14    326.5 18.7  1529  10   US-09-852-156-9    Sequence 9, Appli
15    323   18.5  1083  10   US-09-967-768A-296 Sequence 296, App
16    323   18.5  1427  10   US-09-880-107-3034 Sequence 3034, App
17    321.5 18.4  2268  10   US-09-962-832-218  Sequence 218, App
18    317.5 18.2  2051  10   US-09-944-807-20   Sequence 20, Appl
19    317.5 18.2  2051  10   US-10-084-206-1    Sequence 1, Appli
20    314   18.0  1083  10   US-09-852-156-19   Sequence 19, Appl
21    312.5 17.9  1607   9   US-10-120-394-19   Sequence 19, Appl
22    312.5 17.9  1677  10   US-09-837-446-1    Sequence 1, Appli
23    312   17.9  1408  10   US-09-214-904-5    Sequence 5, Appli
24    311.5 17.8  1753  12   US-10-084-206-1    Sequence 1, Appli
25    311   17.8  1083  10   US-09-852-156-11   Sequence 11, App
26    309   17.7  2061  10   US-09-962-832-239  Sequence 239, App
27    309   17.7  2061  10   US-09-954-456-1593 Sequence 1593, Ap
28    306   17.5  1892   9   US-09-900-699A-1   Sequence 1, Appli
29    304.5 17.4  1896  10   US-09-954-456-959A-1
30    303   17.3  1487  10   US-09-104-792-1    Sequence 1, Appli
31    303   17.3  1487  10   US-09-789-482-3    Sequence 3, Appli
32    303   17.3  1487  10   US-09-789-486-3    Sequence 3, Appli
33    303   17.3  3100  10   US-09-954-456-267  Sequence 267, App
34    303   17.3  3100  10   US-09-954-456-945  Sequence 945, App
35    302   17.3  1910  10   US-09-954-456-1588 Sequence 1588, Ap
36    301.5 17.3  1029  10   US-09-944-807-1    Sequence 1, Appli
37    301.5 17.3  1037  10   US-09-852-156-5    Sequence 5, Appli
38    301.5 17.3  1037  10   US-09-852-156-3    Sequence 3, Appli
39    301   17.2  1689  10   US-09-931-381A-15  Sequence 15, Appl
40    300.5 17.2  1563  10   US-09-880-107-1611 Sequence 1611, Ap
41    299.5 17.1  1717  10   US-09-964-824A-100 Sequence 100, App
42    299.5 17.1  1915  12   US-10-106-623-3    Sequence 3, Appli
43    299.5 17.1  3426   9   US-10-001-833-29   Sequence 29, Appl
44    298.5 17.1  1029  10   US-09-940-063-1    Sequence 1, Appli
45    297   17.0  1143  10   US-09-997-522-1    Sequence 1, Appli
                   1602  10   US-09-804-551B-27  Sequence 27, Appl
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ALIGNMENTS

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RESULT 1
US-09-943-798-3

;  Sequence 3, Application US/09943798
;  Patent No. US2002006521A1
;  GENERAL INFORMATION:
;  APPLICANT: Glaxo Group Limited
;  TITLE OF INVENTION: Polypeptide
;  FILE REFERENCE: QG1021
;  CURRENT APPLICATION NUMBER: US/09/943,798
;  CURRENT FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 4
;  SEQ ID NO 3
;  LENGTH: 1014
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-943-798-3

Alignment Scores:
Pred. No.:              2.5e-41
Score:                  477.00
Percent Similarity:     55.88%           Percent Identity:      
Best Local Similarity:  35.95%
Query Match:            27.30%

US-09-765-034-2 (1-334) x US-09-943-798-3 (1-1014)
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Length:	1014
Matches:	110
Conservative:	61
Mismatches:	123
Indels:	12
Gaps:	6

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Alignment Scores:
Pred. No. :
Score:                  7.24e-33        Length:         831
                        395.50          Matches:         92
Percent Similarity:     55.73%          Conservative:    54
Best Local Similarity:  35.11%          Mismatches:     109
Query Match:            22.64%          Indels:           7
DB:                     10              Gaps:             5
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US-09-765-034-2 (2-334) x US-09-943-798-1 (1-831)

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Qy  52 LeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAla 71
Db   1 ATGAGACCTTGGAAGAGGCAGCCACCATCATTATGTCTGAACCTGGCCTGCACAGAATC 60

Qy  72 PheLeuCysThrLeuProMetLeuIleLeuArgSerTyrAlaAsnGly--AsnTrpIleTyr 90
Db  61 TAYCTGACCAGCCTCCCCTTCCCTGATTCACTACTATGCCAATGGGAAAATGGATCTTT 120

Qy  91 GlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIle 110
Db 121 GGAGATTTCATGTGCATGAGTTAGTTTATCCGCTTCACGTTTACCTGTATATAGCCATC 180

Qy 111 LeuPheLeuThrPheIleSerIleAspArgTyrLeuIleLeuLysTyrProPheArgGlu 130
Db 181 CTCTTCCTCACCGTTCAGCAATCTTGATAGGTTTACCTGTATATTACCCAATGAGCATC 240

Qy 131 HisLeuLeuGlnIleLysLysGlnPheAlaIleLeuIleSerLeuAlaIleTrpValVal 150
Db 241 TTTGACCAGCAAAACTGGATGTGCAGTTGCAGTTGTGCTGTGGATCANTTCA 300

Qy 151 ThrLeuGluLeuProIleLeuLeuAsnProValIleThrArgAspAsnGlyThr 170
Db 301 CTGGTAGCTGTCATTCCAGCGTAGTTTATCCGCTTCTTGATCACACACAACAGACCAACAGATCA 360

Qy 171 ThrCysSerAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCys 190
Db 361 GCCTGCTGCCTCACCAGTTCGGATGAACTCANTACTANTTAAGTGGTACAACCTGATT 420

Qy 191 LeuThrLeuLeuProPheValMetCysPhePheTyrTyrLysIle 210
Db 421 TTGACTGCAACTACTTTGTGCCTCCCCTTGGTAGTAGTGCGATCANTTTTACCTCCATATC 480

Qy 211 AlaLeuPheLeuLysGlnIleValAlaIleThrAlaLeuProLeuGluLysPro 230
Db 481 ---ATCCACACTCTGACCCATGGCAAACTGACAGCGTGCCTTAAG---CAGAAGCA 534

Qy 231 LeuAsnLeuValIleIleMetAlaValAlaValIlePheSerValProPheThr 250
Db 535 CGGAGGCTAACCANTTCTGCTACTCCTTGCATTTTACGTANGTTTTTTACCCTTCCATANTC 594

Qy 251 MetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGlnCysThr--- 269
Db 595 TTGAGGGTCANTTGGATGAAATCTCGCCTGCTTTCA----ATCAGTTGTTCATT 645

Qy 270 GlnValValIleLeuAsnSerPheTyrIleValThrArgProLeuAlaPheLeuAsnSerVal 289
Db 646 GAGAATCAGATCCATGAAGCTTACANCGTTTCNTAGAACTGTGTGCTCTGAACACCTTT 705

Qy 290 IleAsnProValPheTyrPheLeuGlyAspHisPheArgAspMetLeuMetAsnGln 309
Db 706 GGTAACCTGTTACTACTATATGTGGGTGGTCAGCGACGACAACTTTCAGCAGGCTGTCTCTGCTCAACA 765

Qy 310 LeuArg 311
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Qy   8 AsnAlaThrCysLysAsnTrpLeuAlaLeuGluAlaAlaLeuGluLysThrTyrTyrLeuSer 27
Db  67 AATTGCACTGAATGAAAAC------------ATCCCACTCAAGAATGCACTACCTCCCT 111

Qy  28 IlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrLeuAlaValTyrGly 47
Db 112 GTTATTATGGCATTANCTTCCTCGTGGGATTNCCAGNCACTAGTGATATCCACT 171

Qy  48 TyrIlePheSerLeuLysTyrGlyAspValValLeuPheAsnLeuSerVal 67
Db 172 TACATTTTTCAAAATGAGACCTTGGAGAGACAGCCACCATCATTATGTCTGAACCTGCT 231

Qy  68 SerAspLeuAlaPheLeuCysThrLeuProMetLeuIleLeuArgSerTyrAlaAsnGly-- 86
Db 232 ACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCCTGATTCACTACTATGCCAATGGGGAA 291

Qy  87 AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
Db 292 AACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCAATTCAAACCTG 351

Qy 107 TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleLeuLysTyr 126
Db 352 TATACGCAGCATCCTCTTCCTCACCGTTTCAGCATCTTGATAGGTTTACCTGTATATTAC 411

Qy 127 ProPheArgGluHisLeuLeuGlnIleLysLysGlnPheAlaIleLeuIleSerLeuAlaIle 146
Db 412 CCAATGAGCGTGCTTTTCCATTCACAAAAACTGGATGTGCAGTTTGCAGTTGTGCTGTGG 471

Qy 147 TrpValValThrLeuGluLeuProIleLeuLeuAsnProValIleThr 166
Db 472 TGGATCANTTCACTGGGTAGCTGTCATTCCAGCGTAGTTTATCCGCTTCACAACCACAGG 531

Qy 167 AspAsnGlyThrThrCysSerAsnAspPheAlaSerSerGlyAspProAsnTyrAsnLeuIle 186
Db 532 ACCAACAGATCANCGGCTGCTGCCTCACCAGTTCGGATGAACTCANTACTANTTANGTGG 591

Qy 187 TyrSerMetCysLeuThrLeuLeuProPheValMetCysPhePhe 206
Db 592 TACAACCTGATTTGCAACTACTTTGTGCCTCCCCTTGGTAGAAGTGCGATCNTTTCA 651

Qy 207 TyrTyrLysIleAlaLeuPheLeuLysGlnIleValAlaIleThrAlaLeuPro 226
Db 652 TATACCACAGATT---ATCCACACTCTGACCCATGGCAAACTGACAGCGTGCCTTAAG 708

Qy 227 LeuGluLysProLeuAsnLeuValIleIleMetAlaValAlaValIlePheSerValProPheThr 246
Db 709 ---CAGAAGCACGGAGGCTAACCANTTCTGCTACTCCTTGCATTTTACGTANGTTTTTTA 765

Qy 247 ProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyr 266
Db 766 CCCTTCCATANCCTTGAGGGTCANTTGGATGAAATCTCGCCTGCTTTCA----ATC 816

Qy 267 GlnCysThr---GlnValValIleLeuAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
Db 817 AGTTGTTCCANTGAGAATCAGATCCATGAAGCTTACANCGTTTCNTAGAACTGTGTGCT 876

Qy 286 LeuAsnSerValIleAsnProValPheTyrPheLeuGlyAspHisPheArgAspMet 305
Db 877 CTGAACACCTTGTAACCTGTTACTACTATATGTGGGTGGTCAGCGACGACAACTTTCAGCAGGCT 936

Qy 306 LeuMetAsnGlnLeuArg 311
Db 937 GTCTCCTCAACAGTGAGA 954
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Db    766 GTGAGA 771

RESULT 3
US-09-826-791-1
; Sequence 1, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc
; TITLE OF INVENTION: No. US20010039037A1el Polypeptide
; FILE REFERENCE: PC10914ADAM
; CURRENT APPLICATION NUMBER: US/09/826,791
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 008504.3
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/198,367
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 1
; LENGTH: 993
; TYPE: DNA
; ORGANISM: Homo sapiens
; SOFTWARE: Patentin Ver. 2.0
US-09-826-791-1

Alignment Scores:
Pred. No.:
  Score:              1.52e-31
  Percent Similarity: 384.00          Length:         993
  Percent Identity:   47.928          Matches:        102
  Best Local Similarity: 30.36%       Conservative:   59
  Query Match:        21.98%          Mismatches:     125
  DB:                 10              Indels:         50
                                      Gaps:           11

US-09-765-034-2 (1-334) x US-09-826-791-1 (1-993)

Qy    8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr---------  24
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Db   10 AATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA  69

Qy   25 TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal  44
          :::||||||        ||||||||||||:::||
Db   70 TTTTTCCCAATTGTATATCTGATAATATTTTTCTGGGAGTCTTGGGAAATGGGTTGTCC  129

Qy   45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn  64
          |||                          ::::::::::|||
Db  130 ATATATAATGTTTTCCTCCAGCCTTATAAGAAGTCCCACAATCTGTGAACGTTTCATGCTAAAT  189

Qy   65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla  84
          |:||        ::||||||||  |||||||||
Db  190 CTGGGCCATTCAGATCTCCGTGTCATAAGCACGCTTCCCTTCAGGCGTACTATTATCTT  249

Qy   85 AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis  103
          ||| |||            ::|||||||||       ::|||:::
Db  250 AGAGGCTTCCAATTGGAATTTGGAGACCTGGCCTGCAGGATTATTGTCTTAATTCCTTGTAT  309

Qy  104 AlaAsnLeuTyrThrSerIleLeuPheThrPheIleSerIleAlaAspArgTyrLeuIle  123
          |||||||        :::|||||||        ::|:||::
Db  310 GTCACACATGTACAGCAGTATATTATTTCCTGACCGTGCTGTGTTCGTTTCCTGGCA  369

Qy  124 IleLysTyrProPheArg---GluHisLeuLeuGlnLysLysGluPheAlaIleLeuIle  142
          ::|||        |:||||::            ||||||
Db  370 ATGGTTCACCCCTTCGGCTTCTGCATGTCACCAGCATCAGGAGTCGCCTGGAATCCTCTGT  429

Qy  143 SerLeuAlaIleTrpValThrLeuGluLeuProIleLeuProLeuIleAsn  162
          ||||||||||        |||||||||:::|||
Db  430 GGGATC---ATATGGATCCTTATCATGGCTTCCTCAATAATCCTCG------  474

Qy  163 ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn  182
          |||||||||:::::||||||        |||
Db  475 ------------GACAGTGGCTCTGAGCGAAGCGAGTGTCACATCA------  510

Qy  183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu---------  193
          |||||        |||
Db  511 ----------TGCTTAGAGCTGAAATCTCTATAAAAATTGCTAAGCTGCAG  549
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Qy  194 -------------------------LeuGlyPheLeuIleProLeuPheValMetCysPhe  205
                                   :::||||     |||::||||  |||  ::
Db  550 ACCATGAACTATATTGCCTTGGTGGTGGGTGGGCTTGGCCTGCTGCTGCTCATTTTCCACACTTCAGCATC  609

Qy  206 PheTyrTyrLys---IleAlaLeuPheLeuLysGlnArgArgAsnArgGlnValAlaThrAla  224
          |||                     |||::::|||
Db  610 TGTTATCCGTGATCATTCGGTTCTGTTAAAAGTAGAGAGAGTCCCAGAATCGGGGGCTGGG  669

Qy  225 LeuProLeuGluLysProLeuAsnLeuValIleIleMetAlaValValIlePheSerValPro  244
          :::        |||        :::||||||||||||:::||
Db  670 GTTCTCACAGGAGAGGCACTGACCACCATCATCACCACCTTGATCACTCTTCCTGTGT  729

Qy  245 PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys  264
          |||||||||||  :::|||          ||||||:::|||
Db  730 TTCCTGCCCCTATCACACACTGAGGACCGTC----------CACTTGACGACGGAAA  777

Qy  265 GlnTyrGlnCysThrGlnValValIleIleAsnSerPheTyrIleValThrPheArgProLeuAla  284
          |||                 |||||||          :::||||
Db  778 GTGGGTTTATGCAAAGAC---AGACTGCATAAAGCTTTGGTTATCACTACTGGCCCTTGGCA  834

Qy  285 PheLeuAsnSerValIleAsnProValPheTyrProPheLeuLeuGlyAspHisPheArgAsp  304
          |||:::|||                    |||::||||
Db  835 GCAGCCAAAGCCTGCTTCAATCCTCTGCTCTATTACTTTGCTCGGGGAGAATTTAAGGAC  894

Qy  305 MetLeuMetAsnGlnLeuArg------HisAsnPheLysSerLeuThr  318
          |||        :::||||||          ||:::        |||
Db  895 AGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAAGGCAAAGACA  942
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RESULT 4
US-09-828-478-1
; Sequence 1, Application US/09828478
; Patent No. US20020155528A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/09/828,478
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 1
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-828-478-1

Alignment Scores:
Pred. No.:
  Score:              1.62e-31
  Percent Similarity: 384.00          Length:         1041
  Percent Identity:   47.928          Matches:        102
  Best Local Similarity: 30.36%       Conservative:   59
  Query Match:        21.98%          Mismatches:     125
  DB:                 9               Indels:         50
                                      Gaps:           11

US-09-765-034-2 (1-334) x US-09-828-478-1 (1-1041)

Qy    8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr---------  24
          |||        |||                    ||   |:||    ::
Db    8 AATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA  58

Qy   25 TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal  44
          :::||||||        ||||||||||||:::||
Db   58 AATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA  117

Qy   45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn  64
          |||                          ::::::::::|||
Db  118 TTTTTCCCAATTGTATATCTGATAATATTTTTCTGGGAGTCTTGGGAAATGGGTTGTCC  177

Qy   45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn  64
          |||                          ::::::::::|||
Db  178 ATATATAATGTTTTCCTCCAGCCTTATAAGAAGTCCCACAATCTGTGAACGTTTCATGCTAAAT  237
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Qy    65  LeuSerValSerAspLeuValCysThrLeuProMetLeuIleArgSerTyrAla      84
          |||.|:||||.|::||||
Db   238  CTGGCCATTCAGAAGTCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTACTATATCTT  297

Qy    85  AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis 103
          |||     |::||||||.||||:|||||
Db   298  AGAGGCTCCAATTGGATATATTGGAGACGTCCTGCCTGCCAGGATATGTCTTATTCCTTGTAT 357

Qy   104  AlaAsnLeuGlyTyrThrSerIleIleLeuPheLeuGluThrPheIleLeuSerIleLeuAspArgTyrTyrLeuIle 123
Db   358  GTCAACATGTACACCAGTATTATTCTGACCTTTTGTCGGTTGTTCGGCCA          417

Qy   124  IleLysTyrProPheArg---GluHisLeuLeuGlnLysGluProPheAlaIleLeuIle 142
Db   418  ATGGTTCACCCCTTTCGGCTTCACCAGACATCAGGAGTGCCTGGATCCTCTGT        477

Qy   143  SerLeuAlaIleLeuTrpValThrLeuValGluLeuProIleLeuProLeuIleAsn   162
Db   478  GGGATC---ATATGGATCCTTATCATGGCTTCCCAATAATGCTCCTG---          522

Qy   163  ProValIleThrAspAsnGlyThrThrCysSerAsnaspPheAlaSerSerGlyAspProAsn 182
Db   523  -------GACAGTGCCTCGAGCAGAACGCAGAGTGTCACATCA---             558

Qy   183  TyrAsnLeuLeuIleTyrSerMetCysLeuThrLeu---                    193
Db   559  TGCTTAGACTGAATCTCTATAAAATTGCTAAGCTGCAG---                  597

Qy   194  ---LeuGlyPheLeuIleProLeuPheValMetCysPhe                    205
Db   598  ACCATGAACTATATTGCCTTGGTGGGCTGCCTGCCGTTT                    657

Qy   206  PheTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgIleValValAlaThrAla 224
Db   658  TGTTATCTGCTTGATCATTCGGGTTCTGTTAAAAGTGGAGAGTCCCAGAATCGGGGGTCGCG 717

Qy   225  LeuProLeuGluLysProLeuAsnLeuValIleIleMetAlaValValIleIlePheSerValPro 244
Db   718  GTTTCTCACAGGAGGCACTGACCACCATCATCGATCATCTTCTTCTGTGT         777

Qy   245  PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys 264
Db   778  TTCCTGCCCTATCACACACTGAGGAACGTC---                          825

Qy   265  GlnTyrTyrGlnCysThrGlnValValLeuAsnSerPheTyrIleValThrArgProLeuAla 284
Db   826  GTGGGGTTTATGCAAAGAC---AGACTGCATAAAAGTTTGGTTATCACACTGGCCTTGGCA 882

Qy   285  PheLeuAsnSerValIleIleAsnProValPheTyrPheLeuGlyAspHisPheArgAsp 304
Db   883  GCACCCAATGCCTGCTTCAATCCTCTATTACTTTGCTGGGAGAATTTTAAGGAC     942

Qy   305  MetLeuMetAsnGlnLeuArg------HisAsnPheLysSerLeuThr           318
Db   943  AGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAAGGCAAAGACA           990
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Alignment Scores:
Pred. NO.:
Score: 1.62e-31
Score: 384.00
Percent Similarity: 47.92%   Length: 1041
Best Local Similarity: 30.36%   Matches: 102
Query Match: 21.98%   Conservative: 59
DB: 10   Mismatches: 125
                                            Indels: 50
                                            Gaps: 11

US-09-765-034-2 (1-334) x US-09-826-791-5 (1-1041)

```
Qy     8  AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr---      24
          :.||||     :||
Db    58  AATGGCACCTTCAGCAATAACAACAGCAGGAACGCACAATTGAAAACTTCAAGAGAGAA 117

Qy    25  TyrLeuSerIlePheTyrGlyIleLeuGluPheValValGlyValLeuGlyAsnThrIleVal 44
          |||                   |.:|:||||||||
Db   118  TTTTTCCCAATTGTATATATTGGAGACCTGGGAGTCTTGGGAAATGGGGTTGTCC     177

Qy    45  ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64
          |||                   :||
Db   178  ATATATTGGTTTTCTCGAGCCTTATAAGAAGTCCACAATCGTGAAACGTTTTCATGCTAAAT 237

Qy    65  LeuSerValSerAspLeuValAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84
          |||                   :||:||||.|:||||.|::||||
Db   238  CTGGCCATTCAGAATCACAACAGCAGGAACGCACAATTGAAAACTTCAAGAGAGAA   297

Qy    85  AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHis 103
          |||     |::||||||.||||:|||||
Db   298  AGAGGCTCCAATTGGATATATTGGAGACGTCCTGCCTGCCAGGATATGTCTTATTCCTTGTAT 357

Qy   104  AlaAsnLeuGlyTyrThrSerIleIleLeuPheLeuGluThrPheIleLeuSerIleLeuAspArgTyrTyrLeuIle 123
          |||:|:|||||:|:||
Db   358  GTCAACATGTACACCAGTATTATTCTGACCTTTTGTCGGTTGTTCGGCCA          417

Qy   124  IleLysTyrProPheArg---GluHisLeuLeuGlnLysGluProPheAlaIleLeuIle 142
          |||     |.|:
Db   418  ATGGTTCACCCCTTTCGGCTTCACCAGACATCAGGAGTGCCTGGATCCTCTGT       477

Qy   143  SerLeuAlaIleLeuTrpValThrLeuValGluLeuProIleLeuProLeuIleAsn   162
          |||:|:|||:
Db   478  GGGATC---ATATGGATCCTTATCATGGCTTCCCAATAATGCTCCTG---          522

Qy   163  ProValIleThrAspAsnGlyThrThrCysSerAsnaspPheAlaSerSerGlyAspProAsn 182
          |||:|:|||:
Db   523  -------GACAGTGCCTCGAGCAGAACGCAGAGTGTCACATCA---             558

Qy   183  TyrAsnLeuLeuIleTyrSerMetCysLeuThrLeu---                    193
          |||||
Db   559  TGCTTAGACTGAATCTCTATAAAATTGCTAAGCTGCAG---                  597

Qy   194  ---LeuGlyPheLeuIleProLeuPheValMetCysPhe                    205
          |||:|:|:
Db   598  ACCATGAACTATATTGCCTTGGTGGGCTGCCTGCCGTTT                    657

Qy   206  PheTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgIleValValAlaThrAla 224
          |||     :::
Db   658  TGTTATCTGCTTGATCATTCGGGTTCTGTTAAAAGTGGAGAGTCCCAGAATCGGGGGTCGCG 717

Qy   225  LeuProLeuGluLysProLeuAsnLeuValIleIleMetAlaValValIleIlePheSerValPro 244
          |||.:.:
Db   718  GTTTCTCACAGGAGGCACTGACCACCATCATCGATCATCTTCTTCTGTGT         777

Qy   245  PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys 264
          |||||||||||||.::||||
Db   778  TTCCTGCCCTATCACACACTGAGGAACGTC---                          825
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Left column

RESULT 6
US-09-866-230-6
; Sequence 6, Application US/09866230
; Patent No. US2002015090lA1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew, et al.
; TITLE OF INVENTION: No. US2002015090lA1el Nucleic Acids, Polypeptides, Methods of Mak
; FILE REFERENCE: REG 771A
; CURRENT APPLICATION NUMBER: US/09/866,230
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,725
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1041)
US-09-866-230-6

Alignment Scores:
Pred. No.:
Score: 1.62e-31
Score: 384.00
Percent Similarity: 47.92%
Best Local Similarity: 30.36%
Query Match: 21.98%
DB: 10

Length: 1041
Matches: 102
Conservative: 59
Mismatches: 125
Indels: 50
Gaps: 11

US-09-765-034-2 (1-334) x US-09-866-230-6 (1-1041)

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Qy   8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaLeuGluLysTyr-------  24
            |||          :::|||
Db  58 AAtGGCacctTcagcaatAacacagcacaaTTgaaaaacTTcaagagaa       117

Qy  25 TyrLeuSerIlePheTyrGlyIleGluPheValAlaGlyValLeuGlyLysAsnThrIleVal  44
Db 118 TTTTTCCCAAttGtATATCTGAtAaAtATaTTTTCTGGGAGtCTTGGAAAtGGGTTGTCC   177

Qy  45 ValTyrGlyTyrIlePheSerLeuLeuLysAsnTrpPheAsnSerTyrArgLeuPheAsn   64
           |||
Db 178 ATATATGTTTCCTGCAGCCTTATAAGAAGTCCACATCTGAACGTTTTCATGCTAAAT    237

Qy  65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla   84
Db 238 CTGGCCAATTCAGATCCTCCTGTTCATAAGCACGGCTTCCCTTCAGGGCTGACTATTAACTT 297

Qy  85 AsnGly--AsnTrpIleLeuTyrGlyAspValLeuCysLysIleSerGluAsnArgTyrValLeuHis 103
           |||
Db 298 AGAGGCTTCCAATTGGAATAATTGGAGACCTGCGCAGGATTATGTCTTATATCCTTGTAT   357

Qy 104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheLeuSerIleLeuAspArgTyrLeuIle  123
           |||
Db 358 GTCAACAATGTACAGACAGTATTATTTCCTCGACCGTGCTGTTGCGTTTCCTGGCA     417

Qy 124 IleLysTyrProPheArg---GluHisLeuGlnLysLysGluPheAlaIleLeuIle  142
       ::       ::||||||||||
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(continued — alignment of Db 778–990 / Qy 265–318)

```
Db 778 TTCCTGCCTATCACACACTGAGGACGGTC-----------CACTTGACGACATGGAA  825
           ||||||           ||| |||
Qy 265 GlnTyrGlnCysThrGlnValValIleValThrArgProLeuAla           284

Db 826 GTGGGTTTATGCAAAGAC---AGACTGCCATAAAGCTTTGGTTATACACACTGCCCTTGGCA  882
Qy 285 PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp      304

Db 883 GCAGCCAAATGCCTGCTTCAATCCTCTCGTATTACTTGCTGTGGGAGAATTTTAAGGAC  942
Qy 305 MetLeuMetAsnGlnLeuArg------HisAsnPheLysSerLeuThr           318

Db 943 AGACTAAAGTCTGCACTCAGAGAAAAGGCCATCCACAGAGAGGCAAAGACA        990
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Right column

RESULT 7
US-09-828-478-3
; Sequence 3, Application US/09828478
; Patent No. US20020155528A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; TITLE OF INVENTION: Protein
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/09/828,478
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1430
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-828-478-3

Alignment Scores:
Pred. No.:
Score: 2.54e-31
Score: 384.00
Percent Similarity: 47.92%
Best Local Similarity: 30.36%
Query Match: 21.98%
DB:

Length: 1430
Matches: 102
Conservative: 59
Mismatches: 125
Indels: 50
Gaps: 11

```
Db 418 ATGGTTCACCCCTTTCGGCTTCTTGGCATCTGCCATGTCACCAGCATCAGGAGAGTGCCTGGATCCTCTGT 477
Qy 194 -----------LeuGlyPheLeuIlePheLeuProLeuPheValMetCysPhe               205
                   :::||       |||||      |||

Db 478 GGGATC---ATATGGATCCTTTATCATGGCTTCCTTCAATAATGCTCCTG                   522
Qy 143 SerLeuAlaIleIleTrpValLeuValThrLeuGluLeuLeuProIleLeuLeuProLeuIleAsn  162

Db 523 --------GACAGTGGGCTCTGAGCAGAAGACGGCAGTGTCACATCA                      558
Qy 163 ProValIleThrAspAsnGlyThrThrCysAsnAsnPheAlaSerGlyAspAsn              182

Db 559 ----------TGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAG                    597
Qy 183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu-----                             193

Db 598 ACCATGAACTATATATTGCCTTGGTGTGGGCCTGCCTGCTCCCCATTTTTCCACGTCCCATC      657
Qy 206 PheTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaIleThrAla     224

Db 658 TGTTATCTGCTGATCATTCGGGGTTCTGTTAAAAGTGGAGGTCCCAGAANTCGGGGGCTGCGG     717
Qy 225 LeuProLeuGluLysProLeuAsnLeuValAlaIleIleMetAlaValAlaValIlePheSerVal 244

Db 718 GTTTCTCACAGGAGGAGGCACTGACCACCATCAATCAACCTTGATCATCTTCTTCTTGTGT       777
Qy 245 PheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys        264

Db 778 TTCCTGCCTATCACACACTGAGGACGGTC-----------CACTTGACGACATGGAA          825
Qy 265 GlnTyrGlnCysThrGlnValValIleValThrArgProLeuAla                      284

Db 826 GTGGGTTTATGCAAAGAC---AGACTGCCATAAAGCTTTGGTTATACACACTGCCCTTGGCA     882
Qy 285 PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp        304

Db 883 GCAGCCAAATGCCTGCTTCAATCCTCTCGTATTACTTGCTGTGGGAGAATTTTAAGGAC        942
Qy 305 MetLeuMetAsnGlnLeuArg------HisAsnPheLysSerLeuThr                   318

Db 943 AGACTAAAGTCTGCACTCAGAGAAAAGGCCATCCACAGAGAGGCAAAGACA               990
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Left column — Alignment US-09-765-034-2 (1-334) x US-09-828-478-3 (1-1430)

US-09-765-034-2 (1-334) x US-09-828-478-3 (1-1430)

```
Qy      8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr-------- 24
            |||                              ::||||   ::
Db    310 AATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA 369

Qy     25 TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44
            |||::::||||||||||||||||||||||||||||||||||||||   :::
Db    370 TTTTTCCCAAATTGTATAATCTGATAAATATATTTTTCTGGGAGTGCTTTGGAAATGGGTTGTCC 429

Qy     45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64
            |||::||  |||||||||||||||||||||||||::::
Db    430 ATATATAGTTTTTCCTGCAGCCTTATAAGAAACTGCACATCTGTGAAACGTTTCATGCTAAAT 489

Qy     65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84
            |||:::|||||||||||||||||||||||||||||||||||||||||  |||
Db    490 CTGGCCAATTCAGAATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCGTGACTATTATCTT 549

Qy     85 AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerSerAsnArgTyrValLeuHis 103
            :::                |||||||||||||||||||||||||||         ||
Db    550 AGAGGCTCCAATTGGATAATATTGGAGACCTGGCCTGCATCAGGAGAGTGCCTGGAATCCTCTGT 609

Qy    104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIle 123
            ||||||::||||:::::||||||||||||:||||||||||||||
Db    610 GTCAACATGTACAGCAGTATTTATTTCCTGACCGTTCGTGTTCCGTTCCTGGCA 669

Qy    124 IleLysTyrProPheArg---GluHisLeuLeuGlyLysGlyPheAlaIleIleLeuIle 142
            |||                ||||   ::::||||||||||
Db    670 ATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGGTGCCTGGAATCCTCTGT 729

Qy    143 SerLeuAlaIleLeuTrpValLeuValThrLeuGluLeuProIleLeuProLeuLeuAsn 162
            :::                |||||||||:::||||::
Db    730 GGGGATC---ATATGGATCCTTATCATGGGCTTCCTCAATAAATTGCTAAGCTCCTG 774

Qy    183 TyrAsnLeuIleTyrSerMetCysLeuThrLeu-------------------- 193
            |||||||                |||
Db    811 --------------------TGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTCCTG 849

Qy    194 -------------LeuGlyPheLeuIleProLeuPheValMetCysPhe 205
            :::||||||||||||||  :::
Db    850 ACCAGGAAACTATATTGCCCTTGGTGGTGGGGCTGCCGTCGCCATTTTTCACATCAGCATC 909

Qy    206 PheTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAla 224
            |||                |||   :::   |||
Db    910 TGTTAACTTGCTGATCATTTCGGTTCGTTAAAGTGGAGGTCCCCAGAATCGGGCGTGCGG 969

Qy    225 LeuProLeuGluLysProLeuAsnLeuValIleLeuMetAlaValValIlePheSerValPro 244
            :::||                |||||||||||  :::
Db    970 GTTTCTCACAGGAGGCACGTGACCAACATCATCACCTTGATCATCTTTCTTGTGT 1029

Qy    245 PheThrProThrTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLys 264
            |||                :::||||||||||  |||
Db   1030 TTCCTGCCCTATCACACACTGAGGACCGTC--- 1077

Qy    265 GlnTyrGlnCysThrGlnTyrGlnValValIleLeuAsnSerPheTyrIleLeuValThrArgProLeuAla 284
            :::                ||||||   ::::||
Db   1078 GTGGGTTTATCCAAAGAC---AGACTGCATAAAAGCTTTGGTTATCACACTGCCCTTGGCA 1134

Qy    285 PheLeuAsnSerValIleLeuAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAsp 304
            |||||||||||||||||||||||||||||   ::::||
Db   1135 GCAGCCAATGCCTGCTTCAATCCTCGCCTATTACTTTGCTGGGGAGAATTTTAAGGAC 1194

Qy    305 MetLeuMetAsnGlnLeuArg----- 318
            |||||||   :::
Db   1195 AGACTAAAGTCTGCACTCCACAGAAGGCCAAAGACA 1242
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Right column — Alignment US-09-765-034-2 (1-334) x US-09-728-952-26 (1-1700)

Alignment Scores:		
Pred. No.:		
Score:	3.25e-31	Length: 1700
Percent Similarity:	47.92%	Matches: 102
Best Local Similarity:	30.36%	Conservative: 59
Query Match:	21.98%	Mismatches: 125
DB:		Indels: 50 Gaps: 11

US-09-765-034-2 (1-334) x US-09-728-952-26 (1-1700)

```
Qy      8 AsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeuGluLysTyr-------- 24
            |||                              ::||||   ::
Db    289 AATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTCAAGAGAGAA 348

Qy     25 TyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnThrIleVal 44
            |||::::||||||||||||||||||||||||||||||||||||||  :::
Db    349 TTTTTCCCAAATTGTATAATCTGATAAATATATTTTTCTGGGAGTGCTTTGGAAATGGGTTGTCC 408

Qy     45 ValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsn 64
            |||::||  |||||||||||||||||||||||||::::
Db    409 ATATATAGTTTTTCCTGCAGCCTTATAAGAAACTGCACATCTGTGAAACGTTTCATGCTAAAT 468

Qy     65 LeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArgSerTyrAla 84
            |||:::|||||||||||||||||||||||||||||||||||||||||  |||
Db    469 CTGGCCAATTCAGAATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCGTGACTATTATCTT 528

Qy     85 AsnGly---AsnTrpIleTyrGlyAspValLeuCysIleSerSerAsnArgTyrValLeuHis 103
            :::                |||||||||||||||||||||||||||         ||
Db    529 AGAGGCTCCAATTGGATAATATTGGAGACCTGGCCTGCATCAGGAGAGTGCCTGGAATCCTCTGT 588

Qy    104 AlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIle 123
            ||||||::||||:::::||||||||||||:||||||||||||||
Db    589 GTCAACATGTACAGCAGTATTTATTTCCTGACCGTTCGTGTTCCGTTCCTGGCA 648

Qy    124 IleLysTyrProPheArg---GluHisLeuLeuGlyLysGlyPheAlaIleIleLeuIle 142
            |||                ||||   ::::||||||||||
Db    649 ATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGGTGCCTGGAATCCTCTGT 708

Qy    143 SerLeuAlaIleLeuTrpValLeuValThrLeuGluLeuProIleLeuProLeuLeuAsn 162
            :::                |||||||||:::||||::
Db    709 GGGGATC---ATATGGATCCTTATCATGGGCTTCCTCAATAAATTGCTAAGCTCCTG------- 753
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Qy    163  ProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn 182
                |||::::|||:::|||| |||                 :|::|||
Db    754  ------GACAGTGGCTCTGAGCAGAACGGCAGTGTCACATCA----------------- 789

Qy    183  TyrAsnLeuIleTyrSerMetCysLeuThrLeu----------------------- 193
                           |||||||
Db    790  -------TGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAG 828

Qy    194  ---------------------LeuGlyPheLeuIleProLeuPheValMetCysPhe 205
                                 ::::||| |||:::||| |||   :::
Db    829  ACCATGAACTATATTGCCTTGGTGGCTGCTGCCATTTTTCACACTCAGCATC 657

Qy    206  PheTyrTyrLys---IleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThrAla 224
                |||         :: |||||||         :::             |||||:|
Db    889  TGTTATACTGCTGATCATTCGGGTTCTGTTTAAAAGTGGAGGTCCCAGAATCGGGGCTGCGG 948

Qy    225  LeuProLeuGlyLysProLeuAsnLeuValIleMetAlaValAlaValIlePheSerValPro 244
                :::            ||| |||:::||| |||           ::::|||
Db    949  GTTTCTCACAGGAAGGGACTGACCACCATCACCTGATCATTTTTCACACTCAGTGT 888

Qy    245  PheThrProTyrHisValMetArgAsnValArgGlyIleAlaSerArgLeuGlySerTrpLys 264
                ||||||||:|||||       |||||||||:::|||
Db    1009 TTCCTGCCCTATCACACACTGAGGACCGTC----------CACTTGACGACATGGAAA 1056

Qy    265  GlnTyrGlnCysThrGlnValValIleLeuAsnSerPheTyrIleValThrArgProLeuAla 284
                ||||||         |||||:|||               ||:::|||
Db    1057 GTGGGGTTTATGCAAAGAC---AGACTGCCATAAAGCTTGGTATACACACTGCCGCTGGCA 1113

Qy    285  PheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisProheArgAsp 304
                |||:|||||||:::|||                ||||||
Db    1114 GCAGCCAATGCCTGCTTCAATCCTCTGCTATTACTTCGGGGAGAATTTTAAGGAC 1173

Qy    305  MetLeuMetAsnGlnLeuArg-----HisAsnPheLysSerLeuThr 318
                |||||||||             ||||:::
Db    1174 AGACTAAAGTCTGCACTCAGAAAAGGCCATCCAGAGAAGGCAAAGACA 1221
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RESULT 9
US-09-728-422-1

; Sequence 1, Application US/09728422

Patent No. US2002012818751

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: No. US2002012818751Alel Nucleic Acids and
FILE REFERENCE: 787CIP2F
CURRENT APPLICATION NUMBER: US/09/728,422
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 1
LENGTH: 1313
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (547)..(1239)
US-09-728-422-1:

Alignment Scores: Length: 1313

Pred. No.:   2.01e-27   Length: 1313

US-09-765-034-2 (1-334) x US-09-728-422-1 (1-1313)

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Qy      8  AsnAlaThrCysLysAsnTrpLeuAlaLeuAlaGluAlaLeuGluLysThrTyrTyrLeuSer 27
                |||    |||:::            ||||||:::|||:::|||||
Db    613  AATTGCACTGATGAAAAC----------------ATCCCACTCAAGATGCAACTACCTCCCT 657

Qy     28  IleProTyrGlyTyrIleGluPheValGlyValLeuGlyAsnThrIleLeuValThrTyrGly 47
                :::|||||||||          ||||||       :::|||:::|||||
Db    658  GTTATTTATGGCATTATTCTTCCCTCGTGGGAATTCCAGGGAATTGCAGTAGTGATATCCACT 717

Qy     48  TyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerVal 67
                |||||||||||                    |||||||          |||||||
Db    718  TACATTTTCAAAAATGAGACCTTGGGAAGAGCGACCACCATCAATTATGCCAGTGCCGAA 777

Qy     68  SerAspLeuAlaPheLeuCysThrIleLeuProMetIleuAsnArgSerTyrAlaAsnGly--- 86
                    :::                ||||||||||||:::|||||||
Db    778  ACAGAACTGCTGATCATTGACCAGCCTCCCTTCCTGATTCACTTAGCCCTGATTGGCGAA 837

Qy     87  AsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeu 106
                |||||||         |||            |||:::                 ||:::
Db    838  AACTGGATCTATGGAGATTTCATGTGTACTACTACTATGCCAGTGCCGAA 897

Qy    107  TyrThrSerIleLeuPheLeuThrPheIleSerIleAspArgTyrLeuIleIleLysTyr 126
                |||||||:::|||||||||||||||||||            ||||||:::
Db    898  TATACCAGCATCCCTTCCTTCCTCACCTGTTTCAGCATCTTCACTGTGTGGATCAATCAC 957

Qy    127  ProPheArgGluHisIleLeuGlnGlyLysGluPheAlaIleLeuLeuIleSerLeuAlaIle 146
                |||:::|||                ||||||                     ||:::
Db    958  CCAATGAGCTGCTTTTCCATTCACAAAACTGGATGTGCAGTTGTAGCCTGTGCTGGTG 1017

Qy    147  TrpValLeuValThrLeuGluLeuLeuProLeuLeuAsnProValIleThr 166
                |||:::||        :::|||||:::|||||||
Db    1018 TGGATCATTTCACTGTAGCCTGTGCTCATTGACACATCAACCAACACAG 1077

Qy    167  AspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsn---------- 182
                |||   :::   |||      |||:::          :::|||
Db    1078 ACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAAATACTATTAAGGTGG 1137

Qy    183  TyrAsnLeuIleTyrSer-MetCysLeuThrLeuGlyPheLeuIleProLeuPheVa 202
                           |||      |||                ||
Db    1138 TACAACCTAATTTTGACTGCAACTACTTTGCCTC----------CCCTTGGTGAT 1182

Qy    202  IleMetCysPhePheTyrTyrTyrLysIleAla------------------Le 212
                |||            |||
Db    1183 AGTGACACTTTGCTATACCACAGGATTATCCACACTCGACCACATGGACTGCAAACTGACAG 1242

Qy    212  uPheLeuLysGlnArgAsnArgGlnValAlaThrAlaLeu 225
                ||||||||||:::        |||:::
Db    1243 CTGCCTTAAGCAGAAAAGCACGAAGGCTAACCATTCTGCTA 1282
```

RESULT 10
US-09-788-133-1

; Sequence 1, Application US/09788133

Patent No. US2002005200151

GENERAL INFORMATION:

APPLICANT: GLAXO GROUP LTD

TITLE OF INVENTION: ASSAY

FILE REFERENCE: P79011

CURRENT APPLICATION NUMBER: US/09/788,133

CURRENT FILING DATE: 2001-02-20

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 1020

TYPE: DNA

ORGANISM: homo sapiens

FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1)..(1020)
US-09-788-133-1

Alignment Scores:
Pred. No.:
Score:                   1.1e-26
Percent Similarity:      338.00
Best Local Similarity:   48.85%
Query Match:             27.54%
DB:                      19.35%
                         10

US-09-765-034-2 (1-334) x US-09-788-133-1 (1-1020)

Length:                  1020
Matches:                 84
Conservative:            65
Mismatches:              126
Indels:                  30
Gaps:                    6
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```
Qy    18  GluAlaAlaLeuGluLysTyrTyrLeuSerIlePheTyrTyrGlyIleGluPheValValGly  37
              ||||||               ::: |||||               ::|||||:|||:
Db    76  GAGACGCCCACTGGAGAACAGTCGTGTTCGCGCTCCCTTCTACCTTCTGGATTTTATCCTGGCT 135

Qy    38  ValLeuGlyAsnThrIleValValTyrGlyTyrIlePheSerLeuLeuLysAsnTrpAsnSer  57
              :|||||||:|||:::|||||     |||||::: |||     :|||||||||::::
Db   136  TTAGTTGGCAATACCCTTGGCTCTGTGGCTTTTCATCCGAGACCACAAGTCCGGGACCCG 195

Qy    58  SerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuPro  77
             ::||||:|||:: |:|||||||||||||||||||||||:|||:|||     ||
Db   196  GCCAACGTGTTCCTGATGCATCTGGCCGTGCCGGCGACTTGTGTCGTCTGGTTCCTGCCC 255

Qy    78  ---MetLeuIleArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyIleAspValLeuCysIle  96
              |||||         :::|||     ||||| ||:||| ||:     ||||||
Db   256  ACCCGCCTGGTCTACCACTTCTCTGGGAACCACCTGGCCATTGGGGAAAATCCCATGCCGT 315

Qy    97  SerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIle  116
              |||||||||||||||||||||||:     :: |||     ||||||||||||
Db   316  CTCACCCGCCTTCCTCTTTACCTCAACATGTACGCCCAGCCACTTACTTCCTCACCTGCATC 375

Qy   117  SerIleAspArgTyrLeuLeuIleLeuLysTyrProPheArgGluHisLeuLeuGlnLysLys  136
             ||: ||| |||:||||||||||||     |||::|||||     ||: |||
Db   376  AGCGCCGACACCGTTTCCTGGCCATTGTCACCCGGTCAAGTCCCTCAAGCTCCTCCAGGCCC 435

Qy   137  GluPheAlaIleLeuIleSerLeuLeuAlaIleLeuTrpValAlaThrLeuGlnLeuLeuPro  156
             ::|||||         |||||||||||:||||||:||     |||     |||
Db   436  CTCTACGCACACCTGCCCTGTGCCTTCCTCTGTGGGTGGTGGCGTTGGGGCATGGCCCCG 495

Qy   157  IleLeuProLeuIleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAla  176
                |||   |||:||| |||     |||::: |||     |||
Db   496  CTTGCCTGGTGAGCCCACAGACCGTGCAGACCAACACACAGGTGGTCCTGCCTGCAGCGTGTAC 555

Qy   177  SerSerGlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPhe  196
             ::::||:||||     ||||:|||||:::|||||||
Db   556  CGGGAGAAGGCCTCCCACCATGCCCTGGTG---------TCCCTGGCAGTGGCCTTC 603

Qy   197  LeuIleProLeuProPheValMetCysPhePheTyrTyrTyrLysIleAlaLeuPheLeuUlySln  216
                |||         |||     :::|||||||||||:||||:|||
Db   604  ACCTTCCGTCATCACCAGGTTCACTTCTCTTACCTGCTGGATCATCCGCACGTGCCGGCAG 663

Qy   217  ArgAsnArgGlnValAlaThrAlaLeuProLeuGlnLysProLeu------------------ 231
                |||                ::||||||||| |||
Db   664  --------GGCCTCCGTGTGGGACAGCCCCTCAAGACAACAAGGCAGTG 702

Qy   232  AsnLeuValIleMetAlaValValIleProSerValProHeThrProTyrHisValMet 251
             :::::|||     |||||||||||||||||||||||
Db   703  CGCATGATCGGCCATAGTGCCGCCAACTTCCTGGGTCTGCTTCGTGCCTACCACGTCAAC 762

Qy   252  ArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGln--------------- 267
             |||||:|||:|||         :::
Db   763  CGCTCCGGTCTTACGTGCTG-------------------CACTACCGCAGCCATGGGGCC 801

Qy   268  ------CysThrGlnValValIleAsnSerPheTyrIleValThrArgProLeuAlaPhe 285
                    ::|||||     |||
Db   802  TCCTCGGCTCCACCGCATCCTGGCCCCTGGCAAACGCATCACTCCTGCCTCACCAGC 861

Qy   286  LeuAsnSerValIleAsnProValPheTyrPheLeuGlyAspHisPheArgAspMet 305
             |||||| ::: ||||||
Db   862  CTCAACGGGGCACTGACCCCATCANGTATTTCTTCGTGGCTAGGAGAGTTCCGCACGCC 921

Qy   306  LeuMetAsnGlnLeu 310
             |||   ||| |||
Db   922  CTGTGCAACTTGCTC 936
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```
RESULT 11
US-09-864-761-26799/c
Sequence 26799, Application US/09864761
Patent No. US2002004B763A1
GENERAL INFORMATION:
~ APPLICANT: Penn, Sharron G.
~ APPLICANT: Rank, David R.
~ APPLICANT: Hanzel, David K.
~ APPLICANT: Chen, Wensheng
~ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
~ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
~ FILE REFERENCE: Aeomica-X-1
~ CURRENT APPLICATION NUMBER: US/09,864,761
~ CURRENT FILING DATE: 2001-05-23
~ PRIOR APPLICATION NUMBER: US 60/180,312
~ PRIOR FILING DATE: 2000-02-04
~ PRIOR APPLICATION NUMBER: US 60/207,456
~ PRIOR FILING DATE: 2000-05-26
~ PRIOR APPLICATION NUMBER: US 09/632,366
~ PRIOR FILING DATE: 2000-08-03
~ PRIOR APPLICATION NUMBER: GB 24263.6
~ PRIOR FILING DATE: 2000-10-04
~ PRIOR APPLICATION NUMBER: US 60/236,359
~ PRIOR FILING DATE: 2000-09-27
~ PRIOR APPLICATION NUMBER: PCT/US01/00666
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00667
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00664
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00669
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00665
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00668
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00670
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00663
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00662
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: PCT/US01/00661
~ PRIOR FILING DATE: 2001-01-30
~ PRIOR APPLICATION NUMBER: US 09/774,203
~ PRIOR FILING DATE: 2001-01-29
~ NUMBER OF SEQ ID NOS: 49117
~ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
~ SEQ ID NO 26799
~ LENGTH: 1068
~ TYPE: DNA
~ ORGANISM: Homo sapiens
~ FEATURE:
~ OTHER INFORMATION: MAP TO AC007383.2
~ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
~ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
~ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
~ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
~ OTHER INFORMATION: EST_HUMAN HIT: R63760.1, EVALUE 0.00e+00
~ OTHER INFORMATION: NT HIT: gi11430581, EVALUE 0.00e+00
~ OTHER INFORMATION: SWISSPROT HIT: P46091, EVALUE 0.00e+00
; US-09-864-761-26799

Alignment Scores:
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Pred. No.:
Score: 1.69e-26
                        336.50   Length: 1068
Percent Similarity: 47.72%   Matches: 88
Best Local Similarity: 26.75%   Conservative: 69
Query Match: 19.26%   Mismatches: 131
DB: 10   Indels: 41
                                      Gaps: 9

US-09-765-034-2 (1-334) x US-09-864-761-26799 (1-1068)

```
Qy     2 LeuGlyIleMetAlaThrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaAlaLeu   21
           |||||||||::|||||||:::||
Db   945 GCCAGAGTTGTTCACTGGGTCCCCTG------------------------------------   919

Qy    22 GluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsn   41
                                          |||||||:::|||:::::|||||||
Db   876 ----------------------TTCACGGGGTTCAAGTGGAAGAAGACAGTCACCACT   826

Qy    42 ThrIleValValTyrGlyTyrTyrIlePheSerLeuLysAsnTrpAsnSer------SerAsn   59
           |||||||||||:::||                                ::: :::
Db   918 GTGTTATATTGTTTGGCTTTTGTTCTGGGAATTCCAGGAAAT------------SerAsn   877

Qy    60 IleTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeu   79
           |||:||||||||||                ||||
Db   825 CTGTGGTTCCTCAATCTAGCCAATTGCGGATTTCATTTTCTCTTCTTTCGCCCTGTAC   766

Qy    80 IleLeuArgSerTyrAla---AsnGlyAsnTrpIleTyrGlyIleAspValLeuCysIleSerSerAsn   98
           |||     |||       ||| ||||::||||:::
Db   765 ATCTCCTATGGGCCCATGAAATTCCACTGGCCATTGGCCTGTGCAAAGCCAAT   706

Qy    99 ArgTyrValLeuHisIleAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIle   118
           |||:||||                |||||       |||||:::
Db   705 TCCTTCACTGCCCAGTTGAACATGTTTGCCAGTGTTTTTTCCTGACAGTGATCAGCCTG   646

Qy   119 AspArgThrArgLeuIleLeuLysSerTyrProPheArgGluHisIleLeuLeuGlyIleLysLysGluPhe   138
           |||                                      :::
Db   645 GACCACTATATCCACTTGATCCATCCGTCTTATCTCATCGGCATCGAACCCTACAAGAAC   586

Qy   139 AlaIleLeuSerLeuAlaIleLeuTrpValValThrThrLeuGluLeuProIleLeuLeu   158
           |||||||:::|||||||:::::|||||||||||||
Db   585 TCTCTGATTGTCATTATATCATCTGGCTTTTGGCTCCTTCTCTAATTGGCCTGCCCCTG   526

Qy   159 ProLeuIleAsnProValIleThrHisAspAsnGlyThrHisThrCysAsnAspPheAlaSerSer   178
           |||                 ||||||:::
Db   525 TACTTCCGGGACACTGTGGAGTTCAATAATCATCACTCTTTGCTATAACAATTTTCAGAAG   466

Qy   179 GlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThr------------LeuLeu   194
           ::: |||:::|||||||::                         ::: :::
Db   465 CATGATCCTGACCTCACTTTGATCAGGCCACCACGTTCTGACTGGGTGAAAATTTATCATT   406

Qy   195 GlyPheLeuIleProLeuPheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeu   214
           |||:::||||||||||:::                ||| :::
Db   405 GGCTATCTCTTCCCCTTTGCCATGTGTTTCTTCTACTACAAGATAGCTATTGCTAC   352

Qy   215 LysGlnArgAsnArgGlnValAlaThrAlaLeuProLeuGlyLysProLeuAsnLeuVal   234
           |||                  ||||||:::
Db   351 AAGTGAAGAAGGCAAGGCAATC------------CTGATCCTCCAGTAGGCATTTCTGACAATT   301

Qy   235 IleLeuMetAlaValIlePheSerValProPheThrProTyrHisValMetArgAsnVal   254
           |||                        ::: :::|||||||||||||||
Db   300 CTGGTTGTGGTGTGGCCTTTGTGGGTTGCTGGACTCCTTATCACCCTGTTTACGGAACGG   241

Qy   255 ArgIleAlaSerArgLeuGlySerTrpLysGlnTyrArgGlnValValIleIleAsn   274
           :::|||::::|||||||:::                |||||||||||||||:::
Db   240 GAGCTCACCATTCACCACCAAATAGCTATTCCACCAT----------------------   196

Qy   275 SerPheTyrIleValThrArgProLeuAlaPheLeuAsnSerValIleLeuAsnProValPhe   294
           :::                      |||:::
Db   195 GGCTATCTCTTCCCCTTTGCCATGTGTTTCTTCTACAAATGACTATTGCTAC------------   136

Qy   295 TyrPheLeuLeuGlyAspHisPheArgMetLeuMetAsnGlnLeuArgHisAsnPhe   314
           :::||| |||                ||| :::
Db   135 TARGTCTTAATTAAGTAAGAAGTTCCAA------------GCTCGCTTCGGTTCTCAGTT   88
```

RESULT 12

US-09-864-761-10158/c
Sequence 10158, Application US20020048763A1
Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO[R]
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
US-09-864-761-10158

NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 10158
LENGTH: 1422
TYPE: DNA
FEATURE:
ORGANISM: Homo sapiens
OTHER INFORMATION: MAP TO AC007383.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.93
US-09-864-761-10158

Alignment Scores:
Pred. No.:
Score: 2.54e-26
                        336.50   Length: 1422
Percent Similarity: 47.72%   Matches: 88
Best Local Similarity: 26.75%   Conservative: 69
                                      Mismatches: 131

```
Qy   315 LysSerLeuThrSerPheSerArgTrp   323
             :::  ||||||:::::  |||
Db    87 GCTGAGATACTCAAGTACCACACTGTGG   61
```

Query Match:
DB:

19.26%   Indels: 41
10   Gaps: 9

US-09-765-034-2 (1-334) x US-09-864-761-10158 (1-1422)

```
Qy    2 LeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaLaAlaGluAlaAlaLeu     21
        ||||||  |||    ::   |    ||
Db 1218 CTGGGAGTTGTTCACTGGGTCTCCCTG------                                 1192

Qy   22 GluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsn       41
        :::         ||||||||||||||||||
Db 1191 ------GTGTTATATTGTTTGGGCTTTTGTTCTGGGAATTCCAGGAAAT                 1150

Qy   42 ThrIleValThrTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSer-----SerAsn       59
        |||   ||||    ||
Db 1149 GCCATCGTCATTGG----------TTCACGGGGTTCAAGTGGAAGAAGACAGTCACCACT     1099

Qy   60 IleThrTyrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeu     79
        |||||||  ::
Db 1098 CTGTGGGTTCCTCAATCTAGCCATTGCGGATTTCATTTTTCTTCCTTTCTGCCCCTGTAC     1039

Qy   80 IleLeuArgSerTyrAla---AsnGlyAsnTrpIleTyrGlyAspValLeuCysTyrIleSerSerAsn   98
        |||   ::||||   :::||
Db 1038 ATCTCCTATGTGGCCATGAAATTTCCACTGGGCCCTTTGGCATCTGGGCTGTGTGAAAGCCAAT     979

Qy   99 ArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIle       118
        :::
Db  978 TCCTTCACTGCGCAGTTGAACATGTTTTCCCTGACAGTGAATCAGCCTG                 919

Qy  119 AspArgTyrLeuIleIleLysTyrProPheArgGluHisIleLeuLeuGlnLysLysGluPhe     138
        |||||  ::::||
Db  918 GACCACTATATCCACTTGATCCATCCTGTCTTATCTCATCGGCATCCAAGCCCTCAAGAAC     859

Qy  139 AlaIleLeuIleSerLeuAlaIleLeuTrpValValThrLeuGluGluLeuProIleLeu       158
        |||  ||    ::::||
Db  858 TCTCTGATTGTCATTATAATTCATCTGGCCTTTTGGCCTTCTCTAAATTGGCGGTCCTGCCCTG   799

Qy  159 ProLeuIleAsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSer       178
        :::   |||
Db  798 TACTTCCCGGGACACGTGGAGTTCAATAAATCATTACTCTTTGCTATAACAATTTCAGAAG     739

Qy  179 GlyAspProAsnTyrAsnLeuIleTyrSerMetCysLeuThr----------LeuLeu        194
        ||||||  :::::|
Db  738 CATGAATCCTGACCTCACTTGATCAGGCACCACCATGTTCTGACTTGGGGTGAAATTTATCATT   679

Qy  195 GlyPheLeuIleProLeuPheValMetCysPhePheTyrTyrTyrLysIleAlaLeuPheLeu     214
        ||::::||   |||
Db  678 GGCTACTCTCTTTGCTAACAATGAGTATTTGCTAC---------TTGTGTCATCTTC        625

Qy  215 LysGlnArgAsnArgGlnValAlaLaThrAlaLeuProLeuGlyLysProLeuAsnLeuVal     234
        |||   |||
Db  624 AAGGTGAAGAAGCGAAGCATC----------CTGATCTCCAGTAGGCATTTCTGGGACAATT   574

Qy  235 IleMetAlaValAlaIlePheSerValProPheThrProTyrHisValMetArgAsnVal       254
        :::   ||||||
Db  573 CTGGTTGTGGTTGTGGGCCTTTGTGGTTTGCTGGACTCCTTAATCACCTGTTTAGCATTGG     514

Qy  255 ArgIleAlaSerArgLeuGlySerTrpLeuSerTrpGlnTyrGlnCysThrArgGlnValValIleAsn  274
        :::   |||  |||
Db  513 GAGCTCACCCATTCACCACACAAAAGCTATTCCCACCAT---------GTGATGCAG         469

Qy  275 SerPheTyrIleValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPhe       294
        :::
Db  468 GCTGGAATCCCCTCCCACTCGGTTTGGCCATTCCTCAATAGTTGCTTGAACCCCATCCTT     409

Qy  295 TyrPheLeuLeuGlyAspHisPheArgGlyAspMetLeuMetAsnGlnLeuArgHisAsnPhe     314
        |||  |||
Db  408 TATGTCCTAAATTAGTTAAGAAGTTCCAA----------GCTCGCTTCCGGTCCCTCAGTT     361

Qy  315 LysSerLeuThrSerPheSerArgTrp                                       323
        :::  ||
Db  360 GCTGAGAATACTTCAAGTACACACTGTGG                                     334
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Alignment Scores:

Pred. No.:	1.49e-25	Length: 1933
Score:	331.00	Matches: 99
Percent Similarity:	45.19%	Conservative: 56
Best Local Similarity:	28.86%	Mismatches: 143
Query Match:	18.95%	Indels: 45
DB:	9	Gaps: 10

US-09-765-034-2 (1-334) x US-09-104-063-1 (1-1933)

```
Qy   7 TrpAsnAlaThrCysLysAsnTrpLeu----------AlaAlaGlu-AlaAlaLeuGlu      22
       |||  :::||||||||||||  |||   |||
Db 104 TGGCATGCCACCTGCAGATGAAGATTACAGCCCCTGTATGCTAGAAAACTGAGACACTCAA    163

Qy  22 uLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValValGlyValLeuGlyAsnTh    42
       |||||  |||  :::  ||||||||:::|||||||||
Db 164 CAAGTATGTTGTGATCATCGCCTTATGCCCTAGTGTTCCTTGCTGCAAGCCTGCTGGGAAATTC  223

Qy  42 rIleValThrTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyrLe    62
       :::   ||| :::::||||
Db     ...
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CURRENT APPLICATION NUMBER: US/09/880,261
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 09/113,933
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 08/726,575
PRIOR FILING DATE: 1996-10-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 1529
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-880-261-1

Alignment Scores:
Pred. No.:   3.19e-25
Score: 326.50
Percent Similarity: 47.55%
Best Local Similarity: 27.91%
Query Match: 18.69%
DB:

Length: 1529
Matches: 91
Conservative: 64
Mismatches: 134
Indels: 37
Gaps: 10

US-09-765-034-2 (1-334) x US-09-880-261-1 (1-1529)

```
Qy    5  MetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAlaGluAlaGluAlaLeuGluLysTyr  24
             :::||:::|||::|:::
Db  337  ATGGGTAGCAACACGAACGTACCAGCACTGCTGAGATTTACTGTAATGTCACTAATGTGAAATTT  396

Qy   25  TyrLeuSerIlePhe----------TyrGlyIleGluPheValAlaGlyValLeuGlyAsn  41
             ||||:::::|                |||:::  |||:::::|||  |||
Db  397  CAATACTCCCTCTTCAACCACCACTAATCCCTCATATTCAATTCCGGTGCTTCTCTGGCTAAC  456

Qy   42  ThrIleValValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerSerAsnIleTyr  61
             ||||:::  |  |||:::
Db  457  AGTGCAACCGTTGTGGGTTCTGTGCCCCTTCATCAGCAGAAGAAAAATAAAGCCATCAATTTTC  516

Qy   62  LeuPheAsnLeuSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIleArg  81
             ||||||||||||||:::|||||:::  |||||::|:|::|
Db  517  ATGATCAAACCTCTCGTGCTGGGTTCTGACCTTGCTCATGTAATTCTTCCACCCCTCGGAATTAC  576

Qy   82  SerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerSerAsnArgTyrVal  101
             |||:::|||:||||:::||||||||||||||::|||||  |||
Db  577  TATTACATCACGCCACCACTGGCCTTTCCAGAGAGCCCTTCGCTGCTTCTACCTG  636

Qy  102  LeuHisAlaAsnLeuTyrThrHisSerIleLeuPheLeuThrPheIleLeuSerIleAspArgTyr  121
             |||||||||||||
Db  637  AAGTAACTCAACATGTATGCCAGCAATTTGTTTTCCTGACGTGCCATCAGTTCTTCAAAGGTGC  696

Qy  122  LeuIleLeuLysTyrProPheArgGluHisLeuLeuGlyLysLysGluPheAlaIleLeu  141
             ||:||||||||||  :::||
Db  697  TTTTTTCCTCCAGCCCTTCAGGGCCCAGA---GACTGGAAGCGTAGGTACGGAGCTGGGC  753

Qy  142  IleSerLeuAlaIleTrpValThrLeuGluLeuLeuProIleLeuProIleLeu  161
             ||||:::||||:::|:|
Db  754  ATCAGTGCTGCCATCTGGATCGTTGTTGGGGACTGCCTGTTGCCA---TTTCCACATCCTG  810

Qy  162  AsnProValIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspPro  181
             :::|||||  |||
Db  811  AGAAGCACAGACTTAAACAACAACAAGTCCTGC------TTTGCTGATCTTGGATACAAG  864

Qy  182  AsnTyrAsnLeuIleTyrSerMetCysLeu------ThrLeuLeuGlyPheLeu  197
             |||  :::  |||||||||:::
Db  865  CAAAATGAAATCCAGTTGCGTTGCTCGGGATGATGAATTACAGTTGCAGGATTTGTG  924

Qy  198  IleProLeuPheValMetCysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlyAsnArg  217
             :::|||||:::  :::|||  :::||||
Db  925  ATCCCAGTGATCATCATGCGATTGGTGTTACCTGGAAAACTACTATAICCCTGAGACAGCCA  984

Qy  218  AsnArgGlnValAlaThrAlaLeuProLeuAsnLeuValIleMetAla  237
             :::||:  |:::  |||||||  |:::|||
Db  985  CCAATGGCCTTTCCAAGGACTCAGTGAGAGGGAAAGCCACTGCGGGATGGGTTTCATGTGT  1044

Qy  238  ValValIlePheSerValProPheThrProTyrHisVal----------------  250
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Db 1045  GTG  ...
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```
RESULT 15
US-09-852-156-7
Sequence 7, Application US/09852156
Patent No. US2002076694A1
    GENERAL INFORMATION:

    APPLICANT: Littman, Dan R.
               Deng, Hongkui
               Unutmaz, Derya
               Ramani, Vineet N.K.

    TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
                        ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
                        IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
                        THEREOF

    NUMBER OF SEQUENCES: 20

    CORRESPONDENCE ADDRESS:
    ADDRESSEE: David A. Jackson, Esq.
    STREET: 411 Hackensack Ave, Continental Plaza, 4th
            Floor
    CITY: Hackensack
    STATE: New Jersey
    COUNTRY: USA
    ZIP: 07601

    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30

    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/852,156
    FILING DATE: 09-May-2001
    CLASSIFICATION: <Unknown>

    ATTORNEY/AGENT INFORMATION:
    NAME: Jackson Esq., David A.
    REGISTRATION NUMBER: 26,742
    REFERENCE/DOCKET NUMBER: 1049-1-009NCIP

    TELECOMMUNICATION INFORMATION:
    TELEPHONE: 201-487-5800
    TELEFAX: 201-343-1684

    INFORMATION FOR SEQ ID NO: 7:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 1083 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: linear

    MOLECULE TYPE: cDNA
    HYPOTHETICAL: NO
    ORIGINAL SOURCE:
    ORGANISM: Homo sapiens
    SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-852-156-7

Alignment Scores:
Pred. No.:
Score:       4.57e-25      Length:      1083
             323.00        Matches:     83
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```
US-09-765-034-2 (1-334) x US-09-852-156-7 (1-1083)

Percent Similarity:       48.21%      Conservative:     65
Best Local Similarity:    27.04%      Mismatches:      141
Query Match:              18.49%      Indels:           18
DB:                       10          Gaps:              6
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us-09-765-034-2.p2n.rnpb

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